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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/835,107

DATE: 09/06/2001
TIME: 15:59:23

Input Set : A:\sequence listing.txt
Output Set: N:\CRF3\09062001\I835107.raw

ENTERED

<110> APPLICANT: Tudan, Christopher R.
Merzouk, Ahmed
Arab, Lakhdar
Saxena, Geeta
Eaves, Connie J.
Cashman, Johanne
Clark-Lewis
Salari, Hassan
<120> TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
<130> FILE REFERENCE: SMAR012
<140> CURRENT APPLICATION NUMBER: US 09/835,107
C--> <141> CURRENT FILING DATE: 2001-08-20
<150> PRIOR APPLICATION NUMBER: CA 2,305,036
<151> PRIOR FILING DATE: 2000-04-12
<150> PRIOR APPLICATION NUMBER: US 60/232,425
<151> PRIOR FILING DATE: 2000-09-14
<150> PRIOR APPLICATION NUMBER: CA 2,335,109
<151> PRIOR FILING DATE: 2001-02-23
<160> NUMBER OF SEQ ID NOS: 34
<170> SOFTWARE: PatentIn Ver. 2.0
<210> SEQ ID NO: 1
<211> LENGTH: 67
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<223> OTHER INFORMATION: SDF-1 alpha
<400> SEQUENCE: 1

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Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Glu Ser
 1               5                  10                  15
His Val Ala Arg Ala Asn Val Lys His Leu Lys Ile Leu Asn Thr Pro
            20                  25                  30
Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys Asn Asn Asn Arg Gln
        35                  40                  45
Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys
    50                  55                  60
Ala Leu Asn
65
```

<210> SEQ ID NO: 2
<211> LENGTH: 93
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<223> OTHER INFORMATION: SDF-1 Precursor, PBSF
<400> SEQUENCE: 2

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Met Asn Ala Lys Val Val Val Val Leu Val Leu Val Leu Thr Ala Leu
 1               5                  10                  15
Cys Leu Ser Asp Gly Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys
```

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```
129              20                  25                  30
133 Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn Val Lys His Leu Lys
135          35                  40                  45
139 Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys
141      50                  55                  60
145 Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln
147  65                  70                  75                  80
151 Glu Tyr Leu Glu Lys Ala Leu Asn Lys Arg Phe Lys Met
153                  85                  90
159 <210> SEQ ID NO: 3
161 <211> LENGTH: 93
163 <212> TYPE: PRT
165 <213> ORGANISM: Homo sapiens
169 <220> FEATURE:
171 <223> OTHER INFORMATION: SDF-1 beta
175 <400> SEQUENCE: 3
177 Met Asn Ala Lys Val Val Val Val Leu Val Leu Val Leu Thr Ala Leu
179   1               5                  10                  15
183 Cys Leu Ser Asp Gly Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys
185              20                  25                  30
189 Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn Val Lys His Leu Lys
191          35                  40                  45
195 Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys
197      50                  55                  60
201 Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln
203  65                  70                  75                  80
207 Glu Tyr Leu Glu Lys Ala Leu Asn Lys Arg Phe Lys Met
209                  85                  90
215 <210> SEQ ID NO: 4
217 <211> LENGTH: 17
219 <212> TYPE: PRT
221 <213> ORGANISM: Artificial Sequence
225 <220> FEATURE:
227 <223> OTHER INFORMATION: Synthesised in Laboratory: SDF-1(1-17): or
229       CTCE9902
233 <400> SEQUENCE: 4
235 Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Glu Ser
237   1               5                  10                  15
241 His
249 <210> SEQ ID NO: 5
251 <211> LENGTH: 6
253 <212> TYPE: PRT
255 <213> ORGANISM: Artificial Sequence
259 <220> FEATURE:
261 <223> OTHER INFORMATION: Synthesised in Laboratory
265 <400> SEQUENCE: 5
267 Arg Phe Phe Glu Ser His
269   1               5
275 <210> SEQ ID NO: 6
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277 <211> LENGTH: 9
279 <212> TYPE: PRT
281 <213> ORGANISM: Artificial Sequence
285 <220> FEATURE:
287 <223> OTHER INFORMATION: Synthesised in Laboratory
291 <400> SEQUENCE: 6
293 Lys Pro Val Ser Leu Ser Tyr Arg Cys
295 1 5
301 <210> SEQ ID NO: 7
303 <211> LENGTH: 9
305 <212> TYPE: PRT
307 <213> ORGANISM: Artificial Sequence
311 <220> FEATURE:
313 <221> NAME/KEY: DISULFID
315 <222> LOCATION: (9)
317 <223> OTHER INFORMATION: Disulphide linkage between each cys at position 9
319 of each monomer.
323 <220> FEATURE:
325 <223> OTHER INFORMATION: Synthesised in Laboratory:
327 SDF-1(1-9)2-C9/C9-cysteine dimer: or CTCE9901
331 <400> SEQUENCE: 7
333 Lys Pro Val Ser Leu Ser Tyr Arg Cys
335 1 5
341 <210> SEQ ID NO: 8
343 <211> LENGTH: 10
345 <212> TYPE: PRT
347 <213> ORGANISM: Artificial Sequence
351 <220> FEATURE:
353 <221> NAME/KEY: MUTAGEN
355 <222> LOCATION: (10)
357 <223> OTHER INFORMATION: Xaa may be lysine with both the alpha and the
359 epsilon amino groups of the lysine being
361 associated with the covalent (amide) bond
363 formation.
367 <220> FEATURE:
369 <223> OTHER INFORMATION: Synthesised in Laboratory
373 <220> FEATURE:
375 <221> NAME/KEY: VARIANT
377 <222> LOCATION: (10)
379 <223> OTHER INFORMATION: Xaa = a linking moiety between each of the cys at
381 pos. 9 in each SEQ ID Nos: 8 and 9
385 <400> SEQUENCE: 8
387 Lys Pro Val Ser Leu Ser Tyr Arg Cys Xaa
389 1 5 10
395 <210> SEQ ID NO: 9
397 <211> LENGTH: 9
399 <212> TYPE: PRT
401 <213> ORGANISM: Artificial Sequence
405 <220> FEATURE:

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```
407 <223> OTHER INFORMATION: Synthesised in Laboratory
411 <400> SEQUENCE: 9
413 Lys Pro Val Ser Leu Ser Tyr Arg Cys
415   1               5
421 <210> SEQ ID NO: 10
423 <211> LENGTH: 9
425 <212> TYPE: PRT
427 <213> ORGANISM: Artificial Sequence
431 <220> FEATURE:
433 <221> NAME/KEY: MUTAGEN
435 <222> LOCATION: (9)
437 <223> OTHER INFORMATION: Xaa may be lysine with both the alpha and the
439       epsilon amino groups of the lysine being
441       associated with the covalent (amide) bond
443       formation.
447 <220> FEATURE:
449 <223> OTHER INFORMATION: Synthesised in Laboratory
453 <220> FEATURE:
455 <221> NAME/KEY: VARIANT
457 <222> LOCATION: (9)
459 <223> OTHER INFORMATION: Xaa = a linking moiety between each of the arg at
461       pos. 8 in each SEQ ID Nos: 10 and 11
465 <400> SEQUENCE: 10
467 Lys Pro Val Ser Leu Ser Tyr Arg Xaa
469   1               5
475 <210> SEQ ID NO: 11
477 <211> LENGTH: 8
479 <212> TYPE: PRT
481 <213> ORGANISM: Artificial Sequence
485 <220> FEATURE:
487 <223> OTHER INFORMATION: Synthesised in Laboratory
491 <400> SEQUENCE: 11
493 Lys Pro Val Ser Leu Ser Tyr Arg
495   1               5
501 <210> SEQ ID NO: 12
503 <211> LENGTH: 30
505 <212> TYPE: PRT
507 <213> ORGANISM: Artificial Sequence
511 <220> FEATURE:
513 <221> NAME/KEY: DOMAIN
515 <222> LOCATION: (15)..(17)
517 <223> OTHER INFORMATION: spacer monomers (such as the illustrated glycine
519       G's) may be used in variable numbers, such as 2, 3
521       or 4 glycines.
525 <220> FEATURE:
527 <223> OTHER INFORMATION: Synthesised in Laboratory:
529       SDF-1(1-14)-(G)3-SDF-1(55-67) acid
533 <400> SEQUENCE: 12
535 Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Gly Gly
```

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Input Set : A:\sequence listing.txt
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537 1 5 10 15
541 Gly Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu Asn
543 20 25 30
549 <210> SEQ ID NO: 13
551 <211> LENGTH: 31
553 <212> TYPE: PRT
555 <213> ORGANISM: Artificial Sequence
559 <220> FEATURE:
561 <221> NAME/KEY: DOMAIN
563 <222> LOCATION: (16)..(19)
565 <223> OTHER INFORMATION: spacer monomers (such as the illustrated glycine
567 G's) may be used in variable numbers, such as 2, 3
569 or 4 glycines.
573 <220> FEATURE:
575 <223> OTHER INFORMATION: Synthesised in Laboratory:
577 SDF-1(1-14)-(G)4-SDF-1(55-67) acid: or CTCE0013
581 <400> SEQUENCE: 13
583 Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Gly Gly
585 1 5 10 15
589 Gly Gly Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu Asn
591 20 25 30
597 <210> SEQ ID NO: 14
599 <211> LENGTH: 30
601 <212> TYPE: PRT
603 <213> ORGANISM: Artificial Sequence
607 <220> FEATURE:
609 <221> NAME/KEY: DOMAIN
611 <222> LOCATION: (15)..(17)
613 <223> OTHER INFORMATION: spacer monomers (such as the illustrated glycine
615 G's) may be used in variable numbers, such as 2, 3
617 or 4 glycines.
621 <220> FEATURE:
623 <223> OTHER INFORMATION: Synthesised in Laboratory:
625 SDF-1(1-14)-(G)3-SDF-1(55-67) amide
629 <220> FEATURE:
631 <221> NAME/KEY: MOD_RES
633 <222> LOCATION: (30)
635 <223> OTHER INFORMATION: AMIDATION
639 <400> SEQUENCE: 14
641 Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Gly Gly
643 1 5 10 15
647 Gly Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu Asn
649 20 25 30
655 <210> SEQ ID NO: 15
657 <211> LENGTH: 31
659 <212> TYPE: PRT
661 <213> ORGANISM: Artificial Sequence
665 <220> FEATURE:
667 <221> NAME/KEY: DOMAIN

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/835,107

DATE: 09/06/2001
TIME: 15:59:24

Input Set : **A:\sequence listing.txt**
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L:23 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:387 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:467 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10